AMENDMENTS

In the Specification

At page 12, please replace the paragraph beginning on line 1 with the following:

C1

Sequence alignment and homology searches are often determined with the aid of computer methods. A variety of software programs are available in the art. Non-limiting examples of these programs are Blast (available on the worldwide web at http://www. *followed by* ncbi.nlm.nih.gov/BLAST/), Fasta (Genetics Computing Group package, Madison, Wisconsin), DNA Star, MegAlign, and GeneJocky. Any sequence databases that contains DNA sequences corresponding to a gene or a segment thereof can be used for sequence analysis. Commonly employed databases include but are not limited to GenBank, EMBL, DDBJ, PDB, SWISS-PROT, EST, STS, GSS, and HTGS. Sequence similarity can be discerned by aligning the probe sequence against a DNA sequence database. Common parameters for determining the extent of homology set forth by one or more of the aforementioned alignment programs include p value and percent sequence identity. P value is the probability that the alignment is produced by chance. For a single alignment, the p value can be calculated according to Karlin et al. (1990) *Proc.Natl. Acad. Sci* **87**: 2246. For multiple alignments, the p value can be calculated using a heuristic approach such as the one programmed in Blast. Percent sequence identify is defined by the ratio of the number of nucleotide matches between the query sequence and the known sequence when the two are optimally aligned. A probe sequence is considered to have no substantial homology when the region of alignment exhibits less than 20% of sequence identity, more preferably less than 10% identity, even more preferably less than 5% identity using Fasta alignment program with the default settings.

At page 31, please replace the paragraph beginning on line 4 with the following:

C2

Sequence-tagged site (STS) probes (hereinafter STS tags) are generated by amplifying human genomic DNA using selected primer pairs. The selected primer pairs yield amplified sequences corresponding to the 3' untranslated region of gene transcripts of particular interest. A list of exemplary primer pairs and the resultant gene sequences are summarized in Table 1. Additional primer pairs may be obtained from worldwide web at http://www. *followed by* ncbi.nlm.nih.gov/dbSTS/index.html or related web sites. Each PCR reaction contains approximately 100 pmoles of each primer, 50 ng human genomic DNA, and other reagents included in Advantage Genomic PCR kit (Clontech). The PCR reaction is carried out according to manufacturer's instructions which yields approximately 5 ug of each STS tag. The resultant STS tags are analyzed, sequenced, purified, and concentrated by lyophilization (Savant) to approximately 2 ug/ul. Samples of concentrated STS tags are aliquoted and stored at low temperature for future use.